

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: HILLMAN, JENNIFER L.
CORLEY, NEIL C.
PATTERSON, CHANDRA

(ii) TITLE OF INVENTION: HUMAN GLUTATHIONE PEROXIDASE-6

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows
(D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED
(B) FILING DATE: HEREWITH
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Cerrone, Michael C
(B) REGISTRATION NUMBER: 39,132
(C) REFERENCE/DOCKET NUMBER: PF-0530 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-855-0572
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PROSNOT20
(B) CLONE: 1817518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met Val Ala Ala Thr Val Ala Ala Ala Trp Leu Leu Leu Trp Ala Ala
 1           5           10           15
Ala Cys Ala Gln Gln Glu Gln Asp Phe Tyr Asp Phe Lys Ala Val Asn
           20           25           30
Ile Arg Gly Lys Leu Val Ser Leu Glu Lys Tyr Arg Gly Ser Val Ser
           35           40           45
Leu Val Val Asn Val Ala Ser Glu Cys Gly Phe Thr Asp Gln His Tyr
           50           55           60
Arg Ala Leu Gln Gln Leu Gln Arg Asp Leu Gly Pro His His Phe Asn
65           70           75           80
Val Leu Ala Phe Pro Cys Asn Gln Phe Gly Gln Gln Glu Pro Asp Ser
           85           90           95
Asn Lys Glu Ile Glu Ser Phe Ala Cys Arg Thr Tyr Ser Val Ser Phe
           100          105          110
Pro Met Phe Ser Lys Ile Ala Val Thr Gly Thr Gly Ala His Pro Ala
           115          120          125
Phe Lys Tyr Leu Ala Gln Thr Ser Gly Lys Glu Pro Thr Trp Asn Phe
           130          135          140
Trp Lys Tyr Leu Val Ala Pro Asp Gly Lys Val Val Gly Ala Trp Asp
145          150          155          160
Pro Thr Val Ser Val Glu Glu Val Arg Leu Gln Ile Thr Ala Leu Val
           165          170          175
Arg Lys Leu Ile Leu Leu Lys Arg Glu Asp Leu
           180          185

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1072 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT20
- (B) CLONE: 1817518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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GACGCCGCCA CCTCCGGAAC AAGCCATGGT GCGGCGCAGC GTGGCAGCGG CGTGGCTGCT      60
CCTGTGGGCT GCGGCCTGCG CGCAGCAGGA GCAGGACTTC TACGACTTCA AGGCGGTCAA      120
CATCCGGGGC AAACCTGGTGT CGCTGGAGAA GTACCGCGGA TCGGTGTCCC TGGTGGTGAA      180
TGTGGCCAGC GAGTGC GGCT TCACAGACCA GCACTACCGA GCCCTGCAGC AGCTGCAGCG      240
AGACCTGGGC CCCCACCACT TCAACGTGCT CGCCTTCCCC TGCAACCAGT TTGGCCAACA      300
GGAGCCTGAC AGCAACAAGG AGATTGAGAG CTTTGCCTCG CGCACCTACA GTGTCTCATT      360
CCCCATGTTT AGCAAGATTG CAGTCACCGG TACTGGTGCC CATCCTGCCT TCAAGTACCT      420
GGCCCAGACT TCTGGGAAGG AGCCACCTG GAACCTTCTGG AAGTACCTAG TAGCCCCAGA      480
TGGAAGGTG GTAGGGGCTT GGGACCCAAC TGTGTCAGTG GAGGAGGTCA GACTCCAGAT      540
CACAGCGCTC GTGAGGAAGC TCATCCTACT GAAGCGAGAA GACTTATAAC CACCGCGTCT      600
CCTCCTCCAC CACCTCATCC CGCCACCTG TGTGGGGCTG ACCAATGCAA ACTCAAATGG      660
TGCTTCAAAG GGAGAGACCC ACTGACTCTC CTTCCTTTAC TCTTATGCCA TTGGTCCCAT      720
CATTCCTGTG GGGGAAAAAT TCTAGTATTG TGATTATTG AATCTTACAG CAACAAATAG      780
GAACTCCTGG CCAATGAGAG CTCTTGACCA GTGAATCACC AGCCGATACG AACGTCTTGC      840
CAACAAAAAT GTGTGGCAAA TAGAAGTATA TCAAGCAATA ATCTCCCACC CAAGGCTTCT      900
GTAAACTGGG ACCAATGATT ACCTCATAGG GCTGTTGTGA GGATTAGGAT GAAATACCTG      960
TGAAAGTGCC TAGGCAGTGC CAGCCAAATA GGAGGCATTC AATGAACATT TTTTGCATAT     1020
AAACCAAAAA ATAACCTGTT ATCAATAAAA ACTTGCATCC AACATGAATT TC           1072

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GENBANK
- (B) CLONE: 544432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Ala | Ser | Arg | Asp | Asp | Trp | Arg | Cys | Ala | Arg | Ser | Met | His | Glu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Phe | Ser | Ala | Lys | Asp | Ile | Asp | Gly | His | Met | Val | Asn | Leu | Asp | Lys | Tyr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Arg | Gly | Phe | Val | Cys | Ile | Val | Thr | Asn | Val | Ala | Ser | Gln | Cys | Gly | Lys |
| | | | 35 | | | | | 40 | | | | | 45 | | |
| Thr | Glu | Val | Asn | Tyr | Thr | Gln | Leu | Val | Asp | Leu | His | Ala | Arg | Tyr | Ala |
| | | | 50 | | | | 55 | | | | | 60 | | | |
| Glu | Cys | Gly | Leu | Arg | Ile | Leu | Ala | Phe | Pro | Cys | Asn | Gln | Phe | Gly | Lys |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Gln | Glu | Pro | Gly | Ser | Asn | Glu | Glu | Ile | Lys | Glu | Phe | Ala | Ala | Gly | Tyr |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Asn | Val | Lys | Phe | Asp | Met | Phe | Ser | Lys | Ile | Cys | Val | Asn | Gly | Asp | Asp |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ala | His | Pro | Leu | Trp | Lys | Trp | Met | Lys | Ile | Gln | Pro | Lys | Gly | Lys | Gly |
| | | | 115 | | | | | 120 | | | | | 125 | | |
| Ile | Leu | Gly | Asn | Ala | Ile | Lys | Trp | Asn | Phe | Thr | Lys | Phe | Leu | Ile | Asp |
| | | | 130 | | | | 135 | | | | | 140 | | | |
| Lys | Asn | Gly | Cys | Val | Val | Lys | Arg | Tyr | Gly | Pro | Met | Glu | Glu | Pro | Leu |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Val | Ile | Glu | Lys | Asp | Leu | Pro | His | Tyr | Phe | | | | | | |
| | | | | 165 | | | | | 170 | | | | | | |